To: Ms. Nunu Yin

#13

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,221A

DATE: 10/08/2002
TIME: 11:05:25

Input Set : A:\Seqlist.txt
Output Set: N:\CRF4\10082002\I734221A.raw

SEQUENCE LISTING

ENTERED

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 4 (1) GENERAL INFORMATION:
 6         (i) APPLICANT: LITTMAN, DAN R.
 7                        DENG, HONGKUI
 8                        ELLMEIER, WILFRIED
 9                        LANDAU, NATHANIEL R.
10                        LIU, RONG
12        (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
13                        MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
14                        USES THEREOF
16       (iii) NUMBER OF SEQUENCES: 14
18        (iv) CORRESPONDENCE ADDRESS:
19             (A) ADDRESSEE: David A. Jackson, Esq.
20             (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
21                     Floor
22             (C) CITY: Hackensack
23             (D) STATE: New Jersey
24             (E) COUNTRY: USA
25             (F) ZIP: 07601
27         (v) COMPUTER READABLE FORM:
28             (A) MEDIUM TYPE: Floppy disk
29             (B) COMPUTER: IBM PC compatible
30             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
31             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
33        (vi) CURRENT APPLICATION DATA:
C--> 34         (A) APPLICATION NUMBER: US/09/734,221A
C--> 35         (B) FILING DATE: 11-Dec-2000
41             (C) CLASSIFICATION:
C--> 43       (vii) PRIOR APPLICATION DATA:
39             (A) APPLICATION NUMBER: US 08/666,020
40             (B) FILING DATE: 19-JUN-1996
44             (A) APPLICATION NUMBER: US 08/227,319
45             (B) FILING DATE: 13-APR-1994
47      (viii) ATTORNEY/AGENT INFORMATION:
48             (A) NAME: Jackson Esq., David A.
49             (B) REGISTRATION NUMBER: 26,742
50             (C) REFERENCE/DOCKET NUMBER: 1049-1-004 N2
52        (ix) TELECOMMUNICATION INFORMATION:
53             (A) TELEPHONE: 201-487-5800
54             (B) TELEFAX: 201-343-1684
57 (2) INFORMATION FOR SEQ ID NO: 1:
59         (i) SEQUENCE CHARACTERISTICS:
60             (A) LENGTH: 29 base pairs
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61              (B) TYPE: nucleic acid
62              (C) STRANDEDNESS: single
63              (D) TOPOLOGY: linear
65      (ii) MOLECULE TYPE: DNA (genomic)
67     (iii) HYPOTHETICAL: NO
69      (vi) ORIGINAL SOURCE:
70              (A) ORGANISM: Homo sapiens
72..    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 CTCGGATCCG GTGGAACAAG ATGGATTAT                          29
76 (2) INFORMATION FOR SEQ ID NO: 2:
78       (i) SEQUENCE CHARACTERISTICS:
79              (A) LENGTH: 28 base pairs
80              (B) TYPE: nucleic acid
81              (C) STRANDEDNESS: single
82              (D) TOPOLOGY: linear
84      (ii) MOLECULE TYPE: DNA (genomic)
86     (iii) HYPOTHETICAL: NO
88      (vi) ORIGINAL SOURCE:
89              (A) ORGANISM: Homo sapiens
91      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
93 CTCGTCGACA TGTGCACAAC TCTGACTG                           28
96 (2) INFORMATION FOR SEQ ID NO: 3:
98       (i) SEQUENCE CHARACTERISTICS:
99              (A) LENGTH: 66 base pairs
100             (B) TYPE: nucleic acid
101             (C) STRANDEDNESS: double
102             (D) TOPOLOGY: linear
104     (ii) MOLECULE TYPE: cDNA
106    (iii) HYPOTHETICAL: NO
108     (vi) ORIGINAL SOURCE:
109             (A) ORGANISM: Homo sapiens
111     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
113 ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC   60
115 CAAAAA                                                            66
117 (2) INFORMATION FOR SEQ ID NO: 4:
119      (i) SEQUENCE CHARACTERISTICS:
120             (A) LENGTH: 22 amino acids
121             (B) TYPE: amino acid
122             (C) STRANDEDNESS: single
123             (D) TOPOLOGY: linear
125     (ii) MOLECULE TYPE: peptide
127    (iii) HYPOTHETICAL: NO
129      (v) FRAGMENT TYPE: internal
131     (vi) ORIGINAL SOURCE:
132             (A) ORGANISM: Homo sapiens
134     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
136     Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
137     1               5                   10                  15
139     Ser Glu Pro Cys Gln Lys
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140                    20
142 (2) INFORMATION FOR SEQ ID NO: 5:
144       (i) SEQUENCE CHARACTERISTICS:
145            (A) LENGTH: 84 base pairs
146            (B) TYPE: nucleic acid
147            (C) STRANDEDNESS: double
148            (D) TOPOLOGY: linear
150      (ii) MOLECULE TYPE: cDNA
152     (iii) HYPOTHETICAL: NO
155      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
157 ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCCAGAT      60
158 TATGCTTCGG AGCCCTGCCA AAAA                                             84
160 (2) INFORMATION FOR SEQ ID NO: 6:
162       (i) SEQUENCE CHARACTERISTICS:
163            (A) LENGTH: 28 amino acids
164            (B) TYPE: amino acid
165            (C) STRANDEDNESS: single
166            (D) TOPOLOGY: linear
168      (ii) MOLECULE TYPE: peptide
170     (iii) HYPOTHETICAL: NO
171       (v) FRAGMENT TYPE: internal
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
174       Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Pro Tyr
175       1               5                   10                  15
177       Asp Val Pro Asp Tyr Ala Ser Glu Pro Cys Gln Lys
178                       20                  25
180 (2) INFORMATION FOR SEQ ID NO: 7:
182       (i) SEQUENCE CHARACTERISTICS:
183            (A) LENGTH: 51 base pairs
184            (B) TYPE: nucleic acid
185            (C) STRANDEDNESS: single
186            (D) TOPOLOGY: linear
188      (ii) MOLECULE TYPE: other nucleic acid
189            (A) DESCRIPTION: /desc = "Oligonucleotides"
191     (iii) HYPOTHETICAL: NO
193      (vi) ORIGINAL SOURCE:
194            (A) ORGANISM: Homo sapiens
196      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
198 ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A             51
200 (2) INFORMATION FOR SEQ ID NO: 8:
202       (i) SEQUENCE CHARACTERISTICS:
203            (A) LENGTH: 63 base pairs
204            (B) TYPE: nucleic acid
205            (C) STRANDEDNESS: single
206            (D) TOPOLOGY: linear
208      (ii) MOLECULE TYPE: other nucleic acid
209            (A) DESCRIPTION: /desc = "Oligonucleotides"
211     (iii) HYPOTHETICAL: NO
213      (vi) ORIGINAL SOURCE:
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214         (A) ORGANISM: Homo sapiens
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
218 GCAGGATCCA CCATGGATTA TCAAGTGTCA AGTCCAATCT ATGACATCAA TTATCCATAC      60
219 GAT                                                                   63
221 (2) INFORMATION FOR SEQ ID NO: 9:
223     (i) SEQUENCE CHARACTERISTICS:
224         (A) LENGTH: 24 base pairs
225         (B) TYPE: nucleic acid
226         (C) STRANDEDNESS: double
227         (D) TOPOLOGY: linear
229    (ii) MOLECULE TYPE: cDNA
231   (iii) HYPOTHETICAL: NO
234    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
236 CCATACGATG TTCCAGATTA TGCT                                            24
238 (2) INFORMATION FOR SEQ ID NO: 10:
240     (i) SEQUENCE CHARACTERISTICS:
241         (A) LENGTH: 8 amino acids
242         (B) TYPE: amino acid
243         (C) STRANDEDNESS: single
244         (D) TOPOLOGY: linear
246    (ii) MOLECULE TYPE: peptide
248   (iii) HYPOTHETICAL: NO
250     (v) FRAGMENT TYPE: internal
252    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
254      Pro Tyr Asp Val Pro Asp Tyr Ala
255      1               5
257 (2) INFORMATION FOR SEQ ID NO: 11:
259     (i) SEQUENCE CHARACTERISTICS:
260         (A) LENGTH: 30 base pairs
261         (B) TYPE: nucleic acid
262         (C) STRANDEDNESS: single
263         (D) TOPOLOGY: linear
265    (ii) MOLECULE TYPE: cDNA
267   (iii) HYPOTHETICAL: NO
269    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
271 TATCCATACG ATGTTCCAGA TTATGCTTCG                                      30
273 (2) INFORMATION FOR SEQ ID NO: 12:
275     (i) SEQUENCE CHARACTERISTICS:
276         (A) LENGTH: 10 amino acids
277         (B) TYPE: amino acid
278         (C) STRANDEDNESS: single
279         (D) TOPOLOGY: linear
281    (ii) MOLECULE TYPE: peptide
283   (iii) HYPOTHETICAL: NO
285     (v) FRAGMENT TYPE: internal
286    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
288      Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
289      1               5                   10
292 (2) INFORMATION FOR SEQ ID NO: 13:
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PATENT APPLICATION: US/09/734,221A   TIME: 11:05:25

Input Set : A:\Seqlist.txt
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294       (i) SEQUENCE CHARACTERISTICS:
295           (A) LENGTH: 3383 base pairs
296           (B) TYPE: nucleic acid
297           (C) STRANDEDNESS: double
298           (D) TOPOLOGY: linear
300      (ii) MOLECULE TYPE: cDNA
302     (iii) HYPOTHETICAL: NO
304      (vi) ORIGINAL SOURCE:
305           (A) ORGANISM: Homo sapiens
307      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
309 AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAGATGGAT        60
310 TATCAAGTGT CAAGTCCAAT CTATGACATC AATTATTATA CATCGGAGCC CTGCCAAAAA       120
311 ATCAATGTGA AGCAAATCGC AGCCCGCCTC CTGCCTCCGC TCTACTCACT GGTGTTCATC       180
312 TTTGGTTTTG TGGGCAACAT GCTGGTCATC CTCATCCTGA TAAACTGCAA AAGGCTGAAG       240
313 AGCATGACTG ACATCTACCT GCTCAACCTG GCCATCTCTG ACCTGTTTTT CCTTCTTACT       300
314 GTCCCCTTCT GGGCTCACTA TGCTGCCGCC CAGTGGGACT TTGGAAATAC AATGTGTCAA       360
315 CTCTTGACAG GGCTCTATTT TATAGGCTTC TTCTCTGGAA TCTTCTTCAT CATCCTCCTG       420
316 ACAATCGATA GGTACCTGGC TGTCGTCCAT GCTGTGTTTG CTTTAAAAGC CAGGACGGTC       480
317 ACCTTTGGGG TGGTGACAAG TGTGATCACT TGGGTGGTGG CTGTGTTTGC GTCTCTCCCA       540
318 GGAATCATCT TTACCAGATC TCAAAAAGAA GGTCTTCATT ACACCTGCAG CTCTCATTTT       600
319 CCATACAGTC AGTATCAATT CTGGAAGAAT TTCCAGACAT TAAAGATAGT CATCTTGGGG       660
320 CTGGTCCTGC CGCTGCTTGT CATGGTCATC TGCTACTCGG GAATCCTAAA AACTCTGCTT       720
321 CGGTGTCGAA ATGAGAAGAA GAGGCACAGG GCTGTGAGGC TTATCTTCAC CATCATGATT       780
322 GTTTATTTTC TCTTCTGGGC TCCCTACAAC ATTGTCCTTC TCCTGAACAC CTTCCAGGAA       840
323 TTCTTTGGCC TGAATAATTG CAGTAGCTCT AACAGGTTGG ACCAAGCTAT GCAGGTGACA       900
324 GAGACTCTTG GGATGACGCA CTGCTGCATC AACCCCATCA TCTATGCCTT TGTCGGGGAG       960
325 AAGTTCAGAA ACTACCTCTT AGTCTTCTTC CAAAAGCACA TTGCCAAACG CTTCTGCAAA      1020
326 TGCTGTTCTA TTTTCCAGCA AGAGGCTCCC GAGCGAGCAA GCTCAGTTTA CACCCGATCC      1080
327 ACTGGGGAGC AGGAAATATC TGTGGGCTTG TGACACGGAC TCAAGTGGGC TGGTGACCCA      1140
328 GTCAGAGTTG TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGGA      1200
329 GAGGTCTTTT TTAAAAGGAA GTTACTGTTA TAGAGGGTCT AAGATTCATC CATTTATTTG      1260
330 GCATCTGTTT AAAGTAGATT AGATCTTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAA      1320
331 ATATGTTGAT GAAAAATAGC AACCTTTTTA TCTCCCCTTC ACATGCATCA AGTTATTGAC      1380
332 AAACTCTCCC TTCACTCCGA AAGTTCCTTA TGTATATTTA AAAGAAAGCC TCAGAGAATT      1440
333 GCTGATTCTT GAGTTTAGTG ATCTGAACAG AAATACCAAA ATTATTTCAG AAATGTACAA      1500
334 CTTTTTACCT AGTACAAGGC AACATATAGG TTGTAAATGT GTTTAAAACA GGTCTTTGTC      1560
335 TTGCTATGGG GAGAAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCATGTGTG      1620
336 ATTTCCCCTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCAGGC GAGAGACTTG      1680
337 TGGCCTGGGA GAGCTGGGGA AGCTTCTTAA ATGAGAAGGA ATTTGAGTTG GATCATCTAT      1740
338 TGCTGGCAAA GACAGAAGCC TCACTGCAAG CACTGCATGG GCAAGCTTGG CTGTAGAAGG      1800
339 AGACAGAGCT GGTTGGGAAG ACATGGGGAG GAAGGACAAG GCTAGATCAT GAAGAACCTT      1860
340 GACGGCATTG CTCCGTCTAA GTCATGAGCT GAGCAGGGAG ATCCTGGTTG GTGTTGCAGA      1920
341 AGGTTTACTC TGTGGCCAAA GGAGGGTCAG GAAGGATGAG CATTTAGGGC AAGGAGACCA      1980
342 CCAACAGCCC TCAGGTCAGG GTGAGGATGG CCTCTGCTAA GCTCAAGGCG TGAGGATGGG      2040
343 AAGGAGGGAG GTATTCGTAA GGATGGGAAG GAGGGAGGTA TTCGTGCAGC ATATGAGGAT      2100
344 GCAGAGTCAG CAGAACTGGG GTGGATTTGG TTTGGAAGTG AGGGTCAGAG AGGAGTCAGA      2160
345 GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCTTGA AAAGACATCA AGCACAGAAG      2220
346 GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT      2280
347 TGCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTTCACTGA ATGCTTCTGA      2340
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VERIFICATION SUMMARY   DATE: 10/08/2002
PATENT APPLICATION: US/09/734,221A   TIME: 11:05:26

       Input Set : A:\Seqlist.txt
       Output Set: N:\CRF4\10082002\I734221A.raw

L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]